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Sub
C6

-- 14 (amended) A plasmid characterized in that it comprises the luxCDABE genes (SEQ ID NO:3)[,] under transcription control of a tetracycline repressor (TetR) (SEQ ID NO:11) and a tetracycline promoter (TetA) (SEQ ID NO:9) from *Tn10*. --

IN THE SEQUENCE LISTING:

Please substitute the enclosed substitute Sequence Listing for the original Sequence Listing filed as part of the application.

REMARKS

Claims 11 and 14 have been amended to make it clear that the nucleotide sequence encoding a light producing enzyme is under the transcriptional control of a tetracycline repressor and tetracycline promoter. Support for this language can be found in claim 1 as filed. It is believed that these amendments do not constitute new matter and their entry is requested.

A substitute Sequence Listing is being provided. This substitute Sequence Listing differs from the original Sequence Listing filed as part of the application as follows:

- (1) the sequence listing has been prepared to comply with the current rules; and
- (2) the application information has been included.

An appropriate statement under 37 CFR 1.821(f) accompanies this amendment. No new matter is being added and entry of the substitute Sequence Listing is requested.

The Examiner has restricted the claims into three Groups. Applicants traverse this restriction requirement.

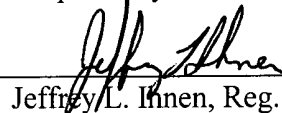
The Examiner contends that the claims in the present application do not relate to a single general inventive concept as required under PCT Rule 13.1. It is believed that the Examiner is in error in this contention, especially as it relates to the amended claims. Applicants first note that neither the International Searching Authority (ISA) or the International Preliminary Examining Authority (IPEA) arrived at the same conclusion of the Examiner. That is, the ISA and the IPEA concluded that the claims complied with PCT Rule 13.1 with respect to unity of invention. Thus, it is believed that the inventions of Groups I-III do relate to a single inventive concept and restriction is improper.

Furthermore, it is submitted that the present claims relate to a single general inventive concept. The gist of the invention is the method of claim 1, i.e., a method to determine the presence of tetracycline in a sample. The method utilizes prokaryotic cells. These prokaryotic cells encompass a DNA vector which includes a nucleotide sequence encoding a light producing enzyme. This nucleotide sequence is under transcriptional control of a tetracycline repressor and a tetracycline promoter. The prokaryotic cell claimed in claim 11 is a cell which encompasses a DNA vector having a light producing enzyme encoding nucleic acid sequence under transcriptional control of a tetracycline repressor and a tetracycline promoter in which the components have been specified according to SEQ ID NOs. The plasmid of claim 14 has a light producing enzyme encoding nucleic acid sequence under transcriptional control of a tetracycline repressor and a tetracycline promoter in which the components have been specified according to SEQ ID NOs. It is evident that the prokaryotic cell of claim 11 and the plasmid of claim 14 have been tailored for use in the method of claim 1. Thus, Applicants submit that all of the claims of the present application related to a single general inventive concept and that restriction is improper.

Applicants provisionally elect Group I for examination with the above noted traverse.

Respectfully submitted,

By



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